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Timestamp: [year=2008; month=1; day=23; hr=13; min=59; sec=56; ms=197;]

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Application No: 10577310 Version No: 1.0

Input Set:

Output Set:

Started: 2008-01-11 10:29:17.804
Finished: 2008-01-11 10:29:18.686
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 882 ms
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Total Errors: 0
No. of SeqIDs Defined: 3
Actual SeqID Count: 3

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (3)

SEQUENCE LISTING

<110> UCHIDA, Yoshiaki
FUJII, Nobuyuki
KURANO, Yoshihiro
OKADA, Masahisa
KOGAKI, Hiroyuki
KIDO, Yasuji

<120> ANTI-SARS VIRUS ANTIBODY, HYBRIDOMA PRODUCING THE
ANTIBODY AND IMMUNOASSAY REAGENT USING THE ANTIBODY

<130> 0760-0354PUS1

<140> 10577310

<141> 2008-01-11

<150> PCT/JP2004/016099

<151> 2004-10-29

<150> JP 2003-373779

<151> 2003-10-31

<150> JP 2004-034268

<151> 2004-02-10

<160> 3

<170> PatentIn version 3.1

 $\langle 210 \rangle$ 1

<211> 1269

<212> DNA

<213> Coronavirus

 $\langle 220 \rangle$

<221> CDS

<222> (1) . . (1269)

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aca ttt ggt gga ccc aca gat tca act gac aat aac cag aat gga gga 96
Thr Phe Gly Gly Pro Thr Asp Ser Thr Asp Asn Asn Gln Asn Gly Gly
20 25 30

cgc aat ggg gca agg cca aaa cag cgc cga ccc caa ggt tta ccc aat 144
 Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn
 35 40 45

aat act gcg tct tgg ttc aca gct ctc act cag cat ggc aag gag gaa 192
Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu
50 55 60

ctt	aga	ttc	cct	cga	ggc	cag	ggc	gtt	cca	atc	aac	acc	aat	agt	ggg	240
Leu	Arg	Phe	Pro	Arg	Gly	Gln	Gly	Val	Pro	Ile	Asn	Thr	Asn	Ser	Gly	
65					70					75					80	
cca	gat	gac	caa	att	ggc	tac	tac	cga	aga	gct	acc	cga	cga	gtt	cgt	288
Pro	Asp	Asp	Gln	Ile	Gly	Tyr	Tyr	Arg	Arg	Ala	Thr	Arg	Arg	Val	Arg	
				85					90					95		
ggt	ggt	gac	ggc	aaa	atg	aaa	gag	ctc	agc	ccc	aga	tgg	tac	ttc	tat	336
Gly	Gly	Asp	Gly	Lys	Met	Lys	Glu	Leu	Ser	Pro	Arg	Trp	Tyr	Phe	Tyr	
			100					105					110			
tac	cta	gga	act	ggc	cca	gaa	gct	tca	ctt	ccc	tac	ggc	gct	aac	aaa	384
Tyr	Leu	Gly	Thr	Gly	Pro	Glu	Ala	Ser	Leu	Pro	Tyr	Gly	Ala	Asn	Lys	
		115					120					125				
gaa	ggc	atc	gta	tgg	gtt	gca	act	gag	gga	gcc	ttg	aat	aca	ccc	aaa	432
Glu	Gly	Ile	Val	Trp	Val	Ala	Thr	Glu	Gly	Ala	Leu	Asn	Thr	Pro	Lys	
	130					135					140					
gac	cac	att	ggc	acc	cgc	aat	cct	aat	aac	aat	gct	gcc	acc	gtg	cta	480
Asp	His	Ile	Gly	Thr	Arg	Asn	Pro	Asn	Asn	Asn	Ala	Ala	Thr	Val	Leu	
145					150					155					160	
caa	ctt	cct	caa	gga	aca	aca	ttg	cca	aaa	ggc	ttc	tac	gca	gag	gga	528
Gln	Leu	Pro	Gln	Gly	Thr	Thr	Leu	Pro	Lys	Gly	Phe	Tyr	Ala	Glu	Gly	
			165						170					175		
agc	aga	ggc	ggc	agt	caa	gcc	tct	tct	cgc	tcc	tca	tca	cgt	agt	cgc	576
Ser	Arg	Gly	Gly	Ser	Gln	Ala	Ser	Ser	Arg	Ser	Ser	Ser	Arg	Ser	Arg	
			180					185					190			
ggt	aat	tca	aga	aat	tca	act	cct	ggc	agc	agt	agg	gga	aat	tct	cct	624
Gly	Asn	Ser	Arg	Asn	Ser	Thr	Pro	Gly	Ser	Ser	Arg	Gly	Asn	Ser	Pro	
		195					200					205				
gct	cga	atg	gct	agc	gga	ggg	ggg	gaa	act	gcc	ctc	gcg	cta	ttg	ctg	672
Ala	Arg	Met	Ala	Ser	Gly	Gly	Gly	Glu	Thr	Ala	Leu	Ala	Leu	Leu	Leu	
	210					215					220					
cta	gac	aga	ttg	aac	cag	ctt	gag	agc	aaa	gtt	tct	ggg	aaa	ggc	caa	720
Leu	Asp	Arg	Leu	Asn	Gln	Leu	Glu	Ser	Lys	Val	Ser	Gly	Lys	Gly	Gln	
225					230					235					240	
caa	caa	caa	ggc	caa	act	gtc	act	aag	aaa	tct	gct	gct	gag	gca	tct	768
Gln	Gln	Gln	Gly	Gln	Thr	Val	Thr	Lys	Lys	Ser	Ala	Ala	Glu	Ala	Ser	
			245						250					255		
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Lys	Lys	Pro	Arg	Gln	Lys	Arg	Thr	Ala	Thr	Lys	Gln	Tyr	Asn	Val	Thr	
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290 295 300	
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Ile Ala Gln Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met Ser Arg	
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Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly	
325 330 335	
gcc att aaa ttg gat gac aaa gat cca caa ttc aaa gac aac gtc ata	1056
Ala Ile Lys Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile	
340 345 350	
ctg ctg aac aag cac att gac gca tac aaa aca ttc cca cca aca gag	1104
Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu	
355 360 365	
cct aaa aag gac aaa aag aaa aag act gat gaa gct cag cct ttg ccg	1152
Pro Lys Lys Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro	
370 375 380	
cag aga caa aag aag cag ccc act gtg act ctt ctt cct gcg gct gac	1200
Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp	
385 390 395 400	
atg gat gat ttc tcc aga caa ctt caa aat tcc atg agt gga gct tct	1248
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gct gat tca act cag gca taa	1269
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 <212> PRT
 <213> Coronavirus

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Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn	
35 40 45	
Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu	
50 55 60	

Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Gly
65 70 75 80

Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg Val Arg
85 90 95

Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr Phe Tyr
100 105 110

Tyr Leu Gly Thr Gly Pro Glu Ala Ser Leu Pro Tyr Gly Ala Asn Lys
115 120 125

Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr Pro Lys
130 135 140

Asp His Ile Gly Thr Arg Asn Pro Asn Asn Asn Ala Ala Thr Val Leu
145 150 155 160

Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala Glu Gly
165 170 175

Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg Ser Arg
180 185 190

Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn Ser Pro
195 200 205

Ala Arg Met Ala Ser Gly Gly Gly Glu Thr Ala Leu Ala Leu Leu Leu
210 215 220

Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln
225 230 235 240

Gln Gln Gln Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser
245 250 255

Lys Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr
260 265 270

Gln Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly
275 280 285

Asp Gln Asp Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln
290 295 300

Ile Ala Gln Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met Ser Arg
305 310 315 320

Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly
325 330 335

Ala Ile Lys Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile
340 345 350

Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu
355 360 365

Pro Lys Lys Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro
370 375 380

Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp
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Met Asp Asp Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser
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Ala Asp Ser Thr Gln Ala
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<210> 3

<211> 18

<212> PRT

<213> Artificial Sequence

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<223> A synthetic peptide sequence consisting of the amino acids
244-260 of SEQ ID NO:2 and Cysteine

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Arg Cys